SEQUENCE LISTING

<110> Bayer AG
      Bayerwerk
      51368 Leverkusen

<120> Regulation of Human Receptor Tyrosine Kinase MerTK

<130> Lio496 WO

<150> US 60/391,933
<151> 2002-06-28

<150> US 60/432,669
<151> 2002-12-12

<160> 21

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 3248
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (101)...(3151)

<400> 1
```
acagggagct tcgctggcgc gcttggccgg cgacaggaca ggttcgggac gtccatctgt  60
ccatccgtcc ggagagaaat tacagatccg cagccccggg atg ggg ccg gcc ccg  115
                                              Met Gly Pro Ala Pro
                                                1               5

ctg ccg ctg ctg ctg ggc ctc ttc ctc ccc gcg ctc tgg cgt aga gct  163
Leu Pro Leu Leu Leu Gly Leu Phe Leu Pro Ala Leu Trp Arg Arg Ala
                10              15                  20

atc act gag gca agg gaa gaa gcc aag cct tac ccg cta ttc ccg gga  211
Ile Thr Glu Ala Arg Glu Glu Ala Lys Pro Tyr Pro Leu Phe Pro Gly
            25              30                  35

cct ttt cca ggg agc ctg caa act gac cac aca ccg ctg tta tcc ctt  259
Pro Phe Pro Gly Ser Leu Gln Thr Asp His Thr Pro Leu Leu Ser Leu
            40              45                  50

cct cac gcc agt ggg tac cag cct gcc ttg atg ttt tca cca acc cag  307
Pro His Ala Ser Gly Tyr Gln Pro Ala Leu Met Phe Ser Pro Thr Gln
    55              60                  65

cct gga aga cca cat aca gga aac gta gcc att ccc cag gtg acc tct  355
Pro Gly Arg Pro His Thr Gly Asn Val Ala Ile Pro Gln Val Thr Ser
    70              75                  80                  85

gtc gaa tca aag ccc cta ccg cct ctt gcc ttc aaa cac aca gtt gga  403
Val Glu Ser Lys Pro Leu Pro Pro Leu Ala Phe Lys His Thr Val Gly
```

```
                    90                  95                  100

cac ata ata ctt tct gaa cat aaa ggt gtc aaa ttt aat tgc tca atc   451
His Ile Ile Leu Ser Glu His Lys Gly Val Lys Phe Asn Cys Ser Ile
            105                 110                 115

agt gta cct aat ata tac cag gac acc aca att tct tgg tgg aaa gat   499
Ser Val Pro Asn Ile Tyr Gln Asp Thr Thr Ile Ser Trp Trp Lys Asp
            120                 125                 130

ggg aag gaa ttg ctt ggg gca cat cat gca att aca cag ttt tat cca   547
Gly Lys Glu Leu Leu Gly Ala His His Ala Ile Thr Gln Phe Tyr Pro
    135                 140                 145

gat gat gaa gtt aca gca ata atc gct tcc ttc agc ata acc agt gtg   595
Asp Asp Glu Val Thr Ala Ile Ile Ala Ser Phe Ser Ile Thr Ser Val
150                 155                 160                 165

cag cgt tca gac aat ggg tcg tat atc tgt aag atg aaa ata aac aat   643
Gln Arg Ser Asp Asn Gly Ser Tyr Ile Cys Lys Met Lys Ile Asn Asn
                170                 175                 180

gaa gag atc gtg tct gat ccc atc tac atc gaa gta caa gga ctt cct   691
Glu Glu Ile Val Ser Asp Pro Ile Tyr Ile Glu Val Gln Gly Leu Pro
            185                 190                 195

cac ttt act aag cag cct gag agc atg aat gtc acc aga aac aca gcc   739
His Phe Thr Lys Gln Pro Glu Ser Met Asn Val Thr Arg Asn Thr Ala
            200                 205                 210

ttc aac ctc acc tgt cag gct gtg ggc ccg cct gag ccc gtc aac att   787
Phe Asn Leu Thr Cys Gln Ala Val Gly Pro Pro Glu Pro Val Asn Ile
            215                 220                 225

ttc tgg gtt caa aac agt agc cgt gtt aac gaa cag cct gaa aaa tcc   835
Phe Trp Val Gln Asn Ser Ser Arg Val Asn Glu Gln Pro Glu Lys Ser
230                 235                 240                 245

ccc tcc gtg cta act gtt cca ggc ctg acg gag atg gcg gtc ttc agt   883
Pro Ser Val Leu Thr Val Pro Gly Leu Thr Glu Met Ala Val Phe Ser
            250                 255                 260

tgt gag gcc cac aat gac aaa ggg ctg acc gtg tcc aag gga gtg cag   931
Cys Glu Ala His Asn Asp Lys Gly Leu Thr Val Ser Lys Gly Val Gln
            265                 270                 275

atc aac atc aaa gca att ccc tcc cca cca act gaa gtc agc atc cgt   979
Ile Asn Ile Lys Ala Ile Pro Ser Pro Pro Thr Glu Val Ser Ile Arg
            280                 285                 290

aac agc act gca cac agc att ctg atc tcc tgg gtt cct ggt ttt gat   1027
Asn Ser Thr Ala His Ser Ile Leu Ile Ser Trp Val Pro Gly Phe Asp
    295                 300                 305

gga tac tcc ccg ttc agg aat tgc agc att cag gtc aag gaa gct gat   1075
Gly Tyr Ser Pro Phe Arg Asn Cys Ser Ile Gln Val Lys Glu Ala Asp
310                 315                 320                 325

ccg ctg agt aat ggc tca gtc atg att ttt aac acc tct gcc tta cca   1123
```

```
Pro Leu Ser Asn Gly Ser Val Met Ile Phe Asn Thr Ser Ala Leu Pro
                330             335           Ser         340

cat ctg tac caa atc aag cag ctg caa gcc ctg gct aat tac agc att     1171
His Leu Tyr Gln Ile Lys Gln Leu Gln Ala Leu Ala Asn Tyr Ser Ile
                345                 350                 355

ggt gtt tcc tgc atg aat gaa ata ggc tgg tct gca gtg agc cct tgg     1219
Gly Val Ser Cys Met Asn Glu Ile Gly Trp Ser Ala Val Ser Pro Trp
                360                 365                 370

att cta gcc agc acg act gaa gga gcc cca tca gta gca cct tta aat     1267
Ile Leu Ala Ser Thr Thr Glu Gly Ala Pro Ser Val Ala Pro Leu Asn
        375                 380                 385

gtc act gtg ttt ctg aat gaa tct agt gat aat gtg gac atc aga tgg     1315
Val Thr Val Phe Leu Asn Glu Ser Ser Asp Asn Val Asp Ile Arg Trp
390                 395                 400                 405

atg aag cct ccg act aag cag cag gat gga gaa ctg gtg ggc tac cgg     1363
Met Lys Pro Pro Thr Lys Gln Gln Asp Gly Glu Leu Val Gly Tyr Arg
                410                 415                 420

ata tcc cac gtg tgg cag agt gca ggg att tcc aaa gag ctc ttg gag     1411
Ile Ser His Val Trp Gln Ser Ala Gly Ile Ser Lys Glu Leu Leu Glu
                425                 430                 435

gaa gtt ggc cag aat ggc agc cga gct cgg atc tct gtt caa gtc cac     1459
Glu Val Gly Gln Asn Gly Ser Arg Ala Arg Ile Ser Val Gln Val His
                440                 445                 450

aat gct acg tgc aca gtg agg att gca gcc gtc acc aga ggg gga gtt     1507
Asn Ala Thr Cys Thr Val Arg Ile Ala Ala Val Thr Arg Gly Gly Val
        455                 460                 465

ggg ccc ttc agt gat cca gtg aaa ata ttt atc cct gca cac ggt tgg     1555
Gly Pro Phe Ser Asp Pro Val Lys Ile Phe Ile Pro Ala His Gly Trp
470                 475                 480                 485

gta gat tat gcc ccc tct tca act ccg gcg cct ggc aac gca gat cct     1603
Val Asp Tyr Ala Pro Ser Ser Thr Pro Ala Pro Gly Asn Ala Asp Pro
                490                 495                 500

gtg ctc atc atc ttt ggc tgc ttt tgt gga ttt att ttg att ggg ttg     1651
Val Leu Ile Ile Phe Gly Cys Phe Cys Gly Phe Ile Leu Ile Gly Leu
                505                 510                 515

att tta tac atc tcc ttg gcc atc aga aaa aga gtc cag gag aca aag     1699
Ile Leu Tyr Ile Ser Leu Ala Ile Arg Lys Arg Val Gln Glu Thr Lys
                520                 525                 530

ttt ggg aat gca ttc aca gag gag gat tct gaa tta gtg gtg aat tat     1747
Phe Gly Asn Ala Phe Thr Glu Glu Asp Ser Glu Leu Val Val Asn Tyr
                535                 540                 545

ata gca aag aaa tcc ttc tgt cgg cga gcc att gaa ctt acc tta cat     1795
Ile Ala Lys Lys Ser Phe Cys Arg Arg Ala Ile Glu Leu Thr Leu His
550                 555                 560                 565
```

- 4 -

```
agc ttg gga gtc agt gag gaa cta caa aat aaa cta gaa gat gtt gtg   1843
Ser Leu Gly Val Ser Glu Glu Leu Gln Asn Lys Leu Glu Asp Val Val
            570             575             580

att gac agg aat ctt cta att ctt gga aaa att ctg ggt gaa gga gag   1891
Ile Asp Arg Asn Leu Leu Ile Leu Gly Lys Ile Leu Gly Glu Gly Glu
            585             590             595

ttt ggg tct gta atg gaa gga aat ctt aag cag gaa gat ggg acc tct   1939
Phe Gly Ser Val Met Glu Gly Asn Leu Lys Gln Glu Asp Gly Thr Ser
            600             605             610

ctg aaa gtg gca gtg aag acc atg aag ttg gac aac tct tca cag cgg   1987
Leu Lys Val Ala Val Lys Thr Met Lys Leu Asp Asn Ser Ser Gln Arg
            615             620             625

gag atc gag gag ttt ctc agt gag gca gcg tgc atg aaa gac ttc agc   2035
Glu Ile Glu Glu Phe Leu Ser Glu Ala Ala Cys Met Lys Asp Phe Ser
630             635             640             645

cac cca aat gtc att cga ctt cta ggt gtg tgt ata gaa atg agc tct   2083
His Pro Asn Val Ile Arg Leu Leu Gly Val Cys Ile Glu Met Ser Ser
            650             655             660

caa ggc atc cca aag ccc atg gta att tta ccc ttc atg aaa tac ggg   2131
Gln Gly Ile Pro Lys Pro Met Val Ile Leu Pro Phe Met Lys Tyr Gly
            665             670             675

gac ctg cat act tac tta ctt tat tcc cga ttg gag aca gga cca aag   2179
Asp Leu His Thr Tyr Leu Leu Tyr Ser Arg Leu Glu Thr Gly Pro Lys
            680             685             690

cat att cct ctg cag aca cta ttg aag ttc atg gtg gat att gcc ctg   2227
His Ile Pro Leu Gln Thr Leu Leu Lys Phe Met Val Asp Ile Ala Leu
            695             700             705

gga atg gag tat ctg agc aac agg aat ttt ctt cat cga gat tta gct   2275
Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe Leu His Arg Asp Leu Ala
710             715             720             725

gct cga aac tgc atc acc cac ctg gcc atc tta gca aga agc cca gca   2323
Ala Arg Asn Cys Ile Thr His Leu Ala Ile Leu Ala Arg Ser Pro Ala
            730             735             740

tct tgc tct tac tgc agg ttg cga gat gac atg act gtc tgt gtt gcg   2371
Ser Cys Ser Tyr Cys Arg Leu Arg Asp Asp Met Thr Val Cys Val Ala
            745             750             755

gac ttc ggc ctc tct aag aag att tac agt ggc gat tat tac cgc caa   2419
Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln
            760             765             770

ggc cgc att gct aag atg cct gtt aaa tgg atc gcc ata gaa agt ctt   2467
Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser Leu
            775             780             785

gca gac cga gtc tac aca agt aaa agt gat gtg tgg gca ttt ggc gtg   2515
Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ala Phe Gly Val
790             795             800             805
```

```
acc atg tgg gaa ata gct acg cgg gga atg act ccc tat cct ggg gtc      2563
Thr Met Trp Glu Ile Ala Thr Arg Gly Met Thr Pro Tyr Pro Gly Val
            810                 815                 820

cag aac cat gag atg tat gac tat ctt ctc cat ggc cac agg ttg aag      2611
Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His Gly His Arg Leu Lys
            825                 830                 835

cag ccc gaa gac tgc ctg gat gaa ctg tat gaa ata atg tac tct tgc      2659
Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Glu Ile Met Tyr Ser Cys
            840                 845                 850

tgg aga acc gat ccc tta gac cgc ccc acc ttt tca gta ttg agg ctg      2707
Trp Arg Thr Asp Pro Leu Asp Arg Pro Thr Phe Ser Val Leu Arg Leu
            855                 860                 865

cag cta gaa aaa ctc tta gaa agt ttg cct gac gtt cgg aac caa gca      2755
Gln Leu Glu Lys Leu Leu Glu Ser Leu Pro Asp Val Arg Asn Gln Ala
870                 875                 880                 885

gac gtt att tac gtc aat aca cag ttg ctg gag agc tct gag ggc ctg      2803
Asp Val Ile Tyr Val Asn Thr Gln Leu Leu Glu Ser Ser Glu Gly Leu
            890                 895                 900

gcc cag ggc tcc acc ctt gct cca ctg gac ttg aac atc gac cct gac      2851
Ala Gln Gly Ser Thr Leu Ala Pro Leu Asp Leu Asn Ile Asp Pro Asp
            905                 910                 915

tct ata att gcc tcc tgc act ccc cgc gct gcc atc agt gtg gtc aca      2899
Ser Ile Ile Ala Ser Cys Thr Pro Arg Ala Ala Ile Ser Val Val Thr
            920                 925                 930

gca gaa gtt cat gac agc aaa cct cat gaa gga cgg tac atc ctg aat      2947
Ala Glu Val His Asp Ser Lys Pro His Glu Gly Arg Tyr Ile Leu Asn
    935                 940                 945

ggg ggc agt gag gaa tgg gaa gat ctg act tct gcc ccc tct gct gca      2995
Gly Gly Ser Glu Glu Trp Glu Asp Leu Thr Ser Ala Pro Ser Ala Ala
950                 955                 960                 965

gtc aca gct gaa aag aac agt gtt tta ccg ggg gag aga ctt gtt agg      3043
Val Thr Ala Glu Lys Asn Ser Val Leu Pro Gly Glu Arg Leu Val Arg
            970                 975                 980

aat ggg gtc tcc tgg tcc cat tcg agc atg ctg ccc ttg gga agc tca      3091
Asn Gly Val Ser Trp Ser His Ser Ser Met Leu Pro Leu Gly Ser Ser
            985                 990                 995

ttg ccc gat gaa ctt ttg ttt gct gac gac tcc tca gaa ggc tca gaa      3139
Leu Pro Asp Glu Leu Leu Phe Ala Asp Asp Ser Ser Glu Gly Ser Glu
            1000                1005                1010

gtc ctg atg tga ggagaggtgc ggggagacat tccaaaaatc aagccaattc        3191
Val Leu Met  *
            1015

ttctgctgta ggagaatcca attgtacctg atgtttttgg tatttgtctt ccttacc      3248
```

```
<210> 2
<211> 1016
<212> PRT
<213> Homo sapiens

<400> 2
Met Gly Pro Ala Pro Leu Pro Leu Leu Leu Gly Leu Phe Leu Pro Ala
 1               5                  10                  15
Leu Trp Arg Arg Ala Ile Thr Glu Ala Arg Glu Glu Ala Lys Pro Tyr
                20                  25                  30
Pro Leu Phe Pro Gly Pro Phe Pro Gly Ser Leu Gln Thr Asp His Thr
            35                  40                  45
Pro Leu Leu Ser Leu Pro His Ala Ser Gly Tyr Gln Pro Ala Leu Met
        50                  55                  60
Phe Ser Pro Thr Gln Pro Gly Arg Pro His Thr Gly Asn Val Ala Ile
65                  70                  75                  80
Pro Gln Val Thr Ser Val Glu Ser Lys Pro Leu Pro Pro Leu Ala Phe
                85                  90                  95
Lys His Thr Val Gly His Ile Ile Leu Ser Glu His Lys Gly Val Lys
            100                 105                 110
Phe Asn Cys Ser Ile Ser Val Pro Asn Ile Tyr Gln Asp Thr Thr Ile
        115                 120                 125
Ser Trp Trp Lys Asp Gly Lys Glu Leu Leu Gly Ala His His Ala Ile
        130                 135                 140
Thr Gln Phe Tyr Pro Asp Asp Glu Val Thr Ala Ile Ile Ala Ser Phe
145                 150                 155                 160
Ser Ile Thr Ser Val Gln Arg Ser Asp Asn Gly Ser Tyr Ile Cys Lys
                165                 170                 175
Met Lys Ile Asn Asn Glu Glu Ile Val Ser Asp Pro Ile Tyr Ile Glu
            180                 185                 190
Val Gln Gly Leu Pro His Phe Thr Lys Gln Pro Glu Ser Met Asn Val
        195                 200                 205
Thr Arg Asn Thr Ala Phe Asn Leu Thr Cys Gln Ala Val Gly Pro Pro
    210                 215                 220
Glu Pro Val Asn Ile Phe Trp Val Gln Asn Ser Ser Arg Val Asn Glu
225                 230                 235                 240
Gln Pro Glu Lys Ser Pro Ser Val Leu Thr Val Pro Gly Leu Thr Glu
                245                 250                 255
Met Ala Val Phe Ser Cys Glu Ala His Asn Asp Lys Gly Leu Thr Val
            260                 265                 270
Ser Lys Gly Val Gln Ile Asn Ile Lys Ala Ile Pro Ser Pro Pro Thr
        275                 280                 285
Glu Val Ser Ile Arg Asn Ser Thr Ala His Ser Ile Leu Ile Ser Trp
    290                 295                 300
Val Pro Gly Phe Asp Gly Tyr Ser Pro Phe Arg Asn Cys Ser Ile Gln
305                 310                 315                 320
Val Lys Glu Ala Asp Pro Leu Ser Asn Gly Ser Val Met Ile Phe Asn
                325                 330                 335
Thr Ser Ala Leu Pro His Leu Tyr Gln Ile Lys Gln Leu Gln Ala Leu
            340                 345                 350
Ala Asn Tyr Ser Ile Gly Val Ser Cys Met Asn Glu Ile Gly Trp Ser
        355                 360                 365
Ala Val Ser Pro Trp Ile Leu Ala Ser Thr Thr Glu Gly Ala Pro Ser
    370                 375                 380
Val Ala Pro Leu Asn Val Thr Val Phe Leu Asn Glu Ser Ser Asp Asn
385                 390                 395                 400
Val Asp Ile Arg Trp Met Lys Pro Pro Thr Lys Gln Gln Asp Gly Glu
                405                 410                 415
Leu Val Gly Tyr Arg Ile Ser His Val Trp Gln Ser Ala Gly Ile Ser
```

- 7 -

```
                    420                    425                    430
Lys Glu Leu Leu Glu Glu Val Gly Gln Asn Gly Ser Arg Ala Arg Ile
            435                    440                    445
Ser Val Gln Val His Asn Ala Thr Cys Thr Val Arg Ile Ala Ala Val
        450                    455                    460
Thr Arg Gly Gly Val Gly Pro Phe Ser Asp Pro Val Lys Ile Phe Ile
465                    470                    475                    480
Pro Ala His Gly Trp Val Asp Tyr Ala Pro Ser Ser Thr Pro Ala Pro
                485                    490                    495
Gly Asn Ala Asp Pro Val Leu Ile Ile Phe Gly Cys Phe Cys Gly Phe
            500                    505                    510
Ile Leu Ile Gly Leu Ile Leu Tyr Ile Ser Leu Ala Ile Arg Lys Arg
        515                    520                    525
Val Gln Glu Thr Lys Phe Gly Asn Ala Phe Thr Glu Glu Asp Ser Glu
        530                    535                    540
Leu Val Val Asn Tyr Ile Ala Lys Lys Ser Phe Cys Arg Arg Ala Ile
545                    550                    555                    560
Glu Leu Thr Leu His Ser Leu Gly Val Ser Glu Glu Leu Gln Asn Lys
                565                    570                    575
Leu Glu Asp Val Val Ile Asp Arg Asn Leu Leu Ile Leu Gly Lys Ile
            580                    585                    590
Leu Gly Glu Gly Glu Phe Gly Ser Val Met Glu Gly Asn Leu Lys Gln
        595                    600                    605
Glu Asp Gly Thr Ser Leu Lys Val Ala Val Lys Thr Met Lys Leu Asp
    610                    615                    620
Asn Ser Ser Gln Arg Glu Ile Glu Glu Phe Leu Ser Glu Ala Ala Cys
625                    630                    635                    640
Met Lys Asp Phe Ser His Pro Asn Val Ile Arg Leu Leu Gly Val Cys
                645                    650                    655
Ile Glu Met Ser Ser Gln Gly Ile Pro Lys Pro Met Val Ile Leu Pro
            660                    665                    670
Phe Met Lys Tyr Gly Asp Leu His Thr Tyr Leu Leu Tyr Ser Arg Leu
        675                    680                    685
Glu Thr Gly Pro Lys His Ile Pro Leu Gln Thr Leu Leu Lys Phe Met
    690                    695                    700
Val Asp Ile Ala Leu Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe Leu
705                    710                    715                    720
His Arg Asp Leu Ala Ala Arg Asn Cys Ile Thr His Leu Ala Ile Leu
            725                    730                    735
Ala Arg Ser Pro Ala Ser Cys Ser Tyr Cys Arg Leu Arg Asp Asp Met
        740                    745                    750
Thr Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly
        755                    760                    765
Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile
    770                    775                    780
Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val
785                    790                    795                    800
Trp Ala Phe Gly Val Thr Met Trp Glu Ile Ala Thr Arg Gly Met Thr
                805                    810                    815
Pro Tyr Pro Gly Val Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His
            820                    825                    830
Gly His Arg Leu Lys Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Glu
        835                    840                    845
Ile Met Tyr Ser Cys Trp Arg Thr Asp Pro Leu Asp Arg Pro Thr Phe
    850                    855                    860
Ser Val Leu Arg Leu Gln Leu Glu Lys Leu Leu Glu Ser Leu Pro Asp
865                    870                    875                    880
Val Arg Asn Gln Ala Asp Val Ile Tyr Val Asn Thr Gln Leu Leu Glu
            885                    890                    895
```

```
Ser Ser Glu Gly Leu Ala Gln Gly Ser Thr Leu Ala Pro Leu Asp Leu
            900                 905                 910
Asn Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr Pro Arg Ala Ala
            915                 920                 925
Ile Ser Val Val Thr Ala Glu Val His Asp Ser Lys Pro His Glu Gly
            930                 935                 940
Arg Tyr Ile Leu Asn Gly Gly Ser Glu Glu Trp Glu Asp Leu Thr Ser
945                 950                 955                 960
Ala Pro Ser Ala Ala Val Thr Ala Glu Lys Asn Ser Val Leu Pro Gly
                965                 970                 975
Glu Arg Leu Val Arg Asn Gly Val Ser Trp Ser His Ser Ser Met Leu
            980                 985                 990
Pro Leu Gly Ser Ser Leu Pro Asp Glu Leu Leu Phe Ala Asp Asp Ser
            995                 1000                1005
Ser Glu Gly Ser Glu Val Leu Met
    1010                1015
```

```
<210> 3
<211> 3048
<212> DNA
<213> Homo sapiens

<400> 3
atggggccgg cccccgctgcc gctgctgctg ggcctcttcc tccccgcgct ctggcgtaga 60
gctatcactg aggcaaggga agaagccaag ccttacccgc tattcccggg accttttcca 120
gggagcctgc aaactgacca cacaccgctg ttatcccttc ctcacgccag tgggtaccag 180
cctgccttga tgttttcacc aacccagcct ggaagaccac atacaggaaa cgtagccatt 240
ccccaggtga cctctgtcga atcaaagccc ctaccgcctc ttgccttcaa acacacagtt 300
ggacacataa tactttctga acataaaggt gtcaaattta attgctcaat cagtgtacct 360
aatatatacc aggacaccac aatttcttgg tggaaagatg ggaaggaatt gcttggggca 420
catcatgcaa ttacacagtt ttatccagat gatgaagtta cagcaataat cgcttccttc 480
agcataacca gtgtgcagcg ttcagacaat gggtcgtata tctgtaagat gaaaataaac 540
aatgaagaga tcgtgtctga tcccatctac atcgaagtac aaggacttcc tcactttact 600
aagcagcctg agagcatgaa tgtcaccaga aacacagcct tcaacctcac ctgtcaggct 660
gtgggcccgc ctgagcccgt caacattttc tgggttcaaa acagtagccg tgttaacgaa 720
cagcctgaaa aatccccctc cgtgctaact gttccaggcc tgacggagat ggcggtcttc 780
agttgtgagg cccacaatga caaaggctg accgtgtcca agggagtgca gatcaacatc 840
aaagcaattc cctccccacc aactgaagtc agcatccgta acagcactgc acacagcatt 900
ctgatctcct gggttcctgg ttttgatgga tactcccgt tcaggaattg cagcattcag 960
gtcaaggaag ctgatccgct gagtaatggc tcagtcatga tttttaacac ctctgcctta 1020
ccacatctgt accaaatcaa gcagctgcaa gccctggcta attacagcat tggtgtttcc 1080
tgcatgaatg aaataggctg gtctgcagtg agcccttgga ttctagccag cacgactgaa 1140
ggagccccat cagtagcacc tttaaatgtc actgtgtttc tgaatgaatc tagtgataat 1200
gtggacatca gatggatgaa gcctccgact aagcagcagg atggagaact ggtgggctac 1260
cggatatccc acgtgtggca gagtgcaggg atttccaaag agctcttgga ggaagttggc 1320
cagaatggca gccgagctcg gatctctgtt caagtccaca atgctacgtg cacagtgagg 1380
attgcagccg tcaccagagg gggagttggg ccttcagtg atccagtgaa aatatttatc 1440
cctgcacacg gttgggtaga ttatgccccc tcttcaactc cggcgcctgg caacgcagat 1500
cctgtgctca tcatctttgg ctgcttttgt ggattatttt gattgggtt gatttatac 1560
atctccttgg ccatcagaaa aagagtccag gagacaaagt ttgggaatgc attcacagag 1620
gaggattctg aattagtggt gaattatata gcaagaaat ccttctgtcg gcgagccatt 1680
gaacttacct tacatagctt gggagtcagt gaggaactac aaaataaact agaagatgtt 1740
gtgattgaca ggaatcttct aattcttgga aaaattctgg gtgaaggaga gtttgggtct 1800
gtaatggaag gaaatcttaa gcaggaagat gggacctctc tgaaagtggc agtgaagacc 1860
atgaagttgg acaactcttc acagcgggag atcgaggagt ttctcagtga ggcagcgtgc 1920
atgaaagact tcagccaccc aaatgtcatt cgacttctag gtgtgtgtat agaaatgagc 1980
tctcaaggca tcccaaagcc catggtaatt ttacccttca tgaaatacgg ggacctgcat 2040
acttacttac tttattcccg attgggagaca ggaccaaagc atattcctct gcagacacta 2100
```

```
ttgaagttca tggtggatat tgccctggga atggagtatc tgagcaacag gaattttctt 2160
catcgagatt tagctgctcg aaactgcatc acccacctgg ccatcttagc aagaagccca 2220
gcatcttgct cttactgcag gttgcgagat gacatgactg tctgtgttgc ggacttcggc 2280
ctctctaaga agatttacag tggcgattat taccgccaag gccgcattgc taagatgcct 2340
gttaaatgga tcgccataga aagtcttgca gaccgagtct acacaagtaa aagtgatgtg 2400
tgggcatttg gcgtgaccat gtgggaaata gctacgcggg gaatgactcc ctatcctggg 2460
gtccagaacc atgagatgta tgactatctt tccatggcc acaggttgaa gcagcccgaa 2520
gactgcctgg atgaactgta tgaaataatg tactcttgct ggagaaccga tcccttagac 2580
cgccccacct tttcagtatt gaggctgcag ctagaaaaac tcttagaaag tttgcctgac 2640
gttcggaacc aagcagacgt tatttacgtc aatacacagt tgctggagag ctctgagggc 2700
ctggcccagg gctccaccct tgctccactg gacttgaaca tcgaccctga tctataatt 2760
gcctcctgca ctccccgcgc tgccatcagt gtggtcacag cagaagttca tgacagcaaa 2820
cctcatgaag gacggtacat cctgaatggg ggcagtgagg aatgggaaga tctgacttct 2880
gcccctctg ctgcagtcac agctgaaaag aacagtgttt taccgggga gagacttgtt 2940
aggaatgggg tctcctggtc ccattcgagc atgctgccct tgggaagctc attgcccgat 3000
gaactttgt ttgctgacga ctcctcagaa ggctcagaag tcctgatg              3048
```

<210> 4
<211> 999
<212> PRT
<213> Homo sapiens

<300>
<308> SWISSPROT/Q12866
<309> 2001-10-16

<400> 4
```
Met Gly Pro Ala Pro Leu Pro Leu Leu Leu Gly Leu Phe Leu Pro Ala
1               5                   10                  15
Leu Trp Arg Arg Ala Ile Thr Glu Ala Arg Glu Glu Ala Lys Pro Tyr
            20                  25                  30
Pro Leu Phe Pro Gly Pro Phe Pro Gly Ser Leu Gln Thr Asp His Thr
            35                  40                  45
Pro Leu Leu Ser Leu Pro His Ala Ser Gly Tyr Gln Pro Ala Leu Met
    50                  55                  60
Phe Ser Pro Thr Gln Pro Gly Arg Pro His Thr Gly Asn Val Ala Ile
65                  70                  75                  80
Pro Gln Val Thr Ser Val Glu Ser Lys Pro Leu Pro Pro Leu Ala Phe
                85                  90                  95
Lys His Thr Val Gly His Ile Ile Leu Ser Glu His Lys Gly Val Lys
            100                 105                 110
Phe Asn Cys Ser Ile Asn Val Pro Asn Ile Tyr Gln Asp Thr Thr Ile
        115                 120                 125
Ser Trp Trp Lys Asp Gly Lys Glu Leu Leu Gly Gly His His Arg Ile
    130                 135                 140
Thr Gln Phe Tyr Pro Asp Asp Glu Val Thr Ala Ile Ile Ala Ser Phe
145                 150                 155                 160
Ser Ile Thr Ser Val Gln Arg Ser Asp Asn Gly Ser Tyr Ile Cys Lys
                165                 170                 175
Met Lys Ile Asn Asn Glu Glu Ile Val Ser Asp Pro Ile Tyr Ile Glu
            180                 185                 190
Val Gln Gly Leu Pro His Phe Thr Lys Gln Pro Glu Ser Met Asn Val
        195                 200                 205
Thr Arg Asn Thr Ala Phe Asn Leu Thr Cys Gln Ala Val Gly Pro Pro
    210                 215                 220
Glu Pro Val Asn Ile Phe Trp Val Gln Asn Ser Ser Arg Val Asn Glu
225                 230                 235                 240
Gln Pro Glu Lys Ser Pro Gly Val Leu Thr Val Pro Gly Leu Thr Glu
                245                 250                 255
```

- 10 -

```
Met Ala Val Phe Ser Cys Glu Ala His Asn Asp Lys Gly Leu Thr Val
        260                 265                 270
Ser Gln Gly Val Gln Ile Asn Ile Lys Ala Ile Pro Ser Pro Pro Thr
        275                 280                 285
Glu Val Ser Ile Arg Asn Ser Thr Ala His Ser Ile Leu Ile Ser Trp
    290                 295                 300
Val Pro Gly Phe Asp Gly Tyr Ser Pro Phe Arg Asn Cys Ser Ile Gln
305                 310                 315                 320
Val Lys Glu Ala Asp Pro Leu Gly Asn Gly Ser Val Met Ile Phe Asn
            325                 330                 335
Thr Ser Ala Leu Pro His Leu Tyr Gln Ile Lys Gln Leu Gln Ala Leu
        340                 345                 350
Ala Asn Tyr Ser Ile Gly Val Ser Cys Met Asn Glu Ile Gly Trp Ser
        355                 360                 365
Ala Val Ser Pro Trp Ile Leu Ala Ser Thr Thr Glu Gly Ala Pro Ser
    370                 375                 380
Val Ala Pro Leu Asn Val Thr Val Phe Leu Asn Glu Ser Ser Asp Asn
385                 390                 395                 400
Val Asp Ile Arg Trp Met Lys Pro Pro Thr Lys Gln Gln Asp Gly Glu
            405                 410                 415
Leu Val Gly Tyr Arg Ile Ser His Val Trp Gln Ser Ala Gly Ile Ser
        420                 425                 430
Lys Glu Leu Leu Glu Glu Val Gly Gln Asn Gly Ser Arg Ala Arg Ile
        435                 440                 445
Ser Val Gln Val His Asn Ala Thr Cys Thr Val Arg Ile Ala Ala Val
    450                 455                 460
Thr Arg Gly Gly Val Gly Pro Phe Ser Asp Pro Val Lys Ile Phe Ile
465                 470                 475                 480
Pro Ala His Gly Trp Val Asp Tyr Ala Pro Ser Ser Thr Pro Ala Pro
            485                 490                 495
Gly Asn Ala Asp Pro Val Leu Ile Ile Phe Gly Cys Phe Cys Gly Phe
        500                 505                 510
Ile Leu Ile Gly Leu Ile Leu Tyr Ile Ser Leu Ala Ile Arg Lys Arg
        515                 520                 525
Val Gln Glu Thr Lys Phe Gly Asn Ala Phe Thr Glu Glu Asp Ser Glu
    530                 535                 540
Leu Val Val Asn Tyr Ile Ala Lys Lys Ser Phe Cys Arg Arg Ala Ile
545                 550                 555                 560
Glu Leu Thr Leu His Ser Leu Gly Val Ser Glu Glu Leu Gln Asn Lys
            565                 570                 575
Leu Glu Asp Val Val Ile Asp Arg Asn Leu Leu Ile Leu Gly Lys Ile
            580                 585                 590
Leu Gly Glu Gly Glu Phe Gly Ser Val Met Glu Gly Asn Leu Lys Gln
        595                 600                 605
Glu Asp Gly Thr Ser Leu Lys Val Ala Val Lys Thr Met Lys Leu Asp
    610                 615                 620
Asn Ser Ser His Arg Glu Ile Glu Glu Phe Leu Ser Glu Ala Ala Cys
625                 630                 635                 640
Met Lys Asp Phe Ser His Pro Asn Val Ile Arg Leu Leu Gly Val Cys
            645                 650                 655
Ile Glu Met Ser Ser Gln Gly Ile Pro Lys Pro Met Val Ile Leu Pro
            660                 665                 670
Phe Met Lys Tyr Gly Asp Leu His Thr Tyr Leu Leu Tyr Ser Arg Leu
        675                 680                 685
Glu Thr Gly Pro Lys His Ile Pro Leu Gln Thr Leu Leu Lys Phe Met
    690                 695                 700
Val Asp Ile Ala Leu Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe Leu
705                 710                 715                 720
His Arg Asp Leu Ala Ala Arg Asn Cys Met Leu Arg Asp Asp Met Thr
```

```
                    725                    730                    735
Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly Asp
                740                    745                    750
Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala
                755                    760                    765
Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp
            770                    775                    780
Ala Phe Gly Val Thr Met Trp Glu Ile Arg Thr Arg Gly Met Thr Pro
785                    790                    795                    800
Tyr Pro Gly Val Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His Gly
                805                    810                    815
His Arg Leu Lys Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Glu Ile
                820                    825                    830
Met Tyr Ser Cys Trp Arg Thr Asp Pro Leu Asp Arg Pro Thr Phe Ser
                835                    840                    845
Val Leu Arg Leu Gln Leu Glu Lys Leu Leu Glu Ser Leu Pro Asp Val
    850                    855                    860
Arg Asn Gln Ala Asp Val Ile Tyr Val Asn Thr Gln Leu Leu Glu Ser
865                    870                    875                    880
Ser Glu Gly Leu Ala Gln Gly Pro Thr Leu Ala Pro Leu Asp Leu Asn
                885                    890                    895
Ile Asp Pro Asp Ser Ile Ile Ala Ser Cys Thr Pro Arg Ala Ala Ile
                900                    905                    910
Ser Val Val Thr Ala Glu Val His Asp Ser Lys Pro His Glu Gly Arg
                915                    920                    925
Tyr Ile Leu Asn Gly Gly Ser Glu Glu Trp Glu Asp Leu Thr Ser Ala
                930                    935                    940
Pro Ser Ala Ala Val Thr Ala Glu Lys Asn Ser Val Leu Pro Gly Glu
945                    950                    955                    960
Arg Leu Val Arg Asn Gly Val Ser Trp Ser His Ser Ser Met Leu Pro
                965                    970                    975
Leu Gly Ser Ser Leu Pro Asp Glu Leu Leu Phe Ala Asp Asp Ser Ser
                980                    985                    990
Glu Gly Ser Glu Val Leu Met
                995
```

```
<210> 5
<211> 235
<212> PRT
<213> Homo sapiens

<400> 5
Thr Gly Pro Lys His Ile Pro Leu Gln Thr Leu Trp Lys Phe Met Val
1                   5                    10                   15
Asp Ile Ala Leu Gly Met Glu Tyr Leu Ser Asn Arg Asn Phe Leu His
            20                    25                    30
Arg Asp Leu Ala Ala Arg Asn Cys Ile Thr His Leu Ala Ile Leu Ala
            35                    40                    45
Arg Ser Pro Ala Ser Cys Ser Tyr Cys Arg Leu Arg Asp Asp Met Thr
        50                    55                    60
Val Cys Val Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly Asp
65                    70                    75                    80
Tyr Tyr Arg Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala
                85                    90                    95
Ile Glu Ser Leu Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp
            100                   105                   110
Ala Phe Gly Val Thr Met Trp Glu Asp Asp Met Thr Val Cys Val Ala
        115                   120                   125
```

- 12 -

```
Asp Phe Gly Leu Ser Lys Lys Ile Tyr Ser Gly Asp Tyr Tyr Arg Gln
    130                 135                 140
Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser Leu
145                 150                 155                 160
Ala Asp Arg Val Tyr Thr Ser Lys Ser Asp Val Trp Ala Phe Gly Val
                165                 170                 175
Thr Met Trp Glu Ile Ala Thr Arg Gly Met Thr Pro Tyr Pro Gly Val
            180                 185                 190
Gln Asn His Glu Met Tyr Asp Tyr Leu Leu His Gly His Arg Leu Lys
        195                 200                 205
Gln Pro Glu Asp Cys Leu Asp Glu Leu Tyr Glu Ile Met Tyr Ser Cys
    210                 215                 220
Trp Arg Thr Asp Pro Leu Asp Arg Pro Pro Phe
225                 230                 235
```

```
<210> 6
<211> 830
<212> DNA
<213> Homo sapiens

<400> 6
cgggatcgat tattaccgcc aaggccgcat tgctaagatg cctgttaaat ggatcgccat 60
aggaaggtct tgcagaccga gtctacacaa gtaaaagtga tgtgtgggca tttggcgtga 120
ccatgtggga aatagctacg cggggaatga ctccctatcc tggggtccag aaccatgaga 180
tgtatgacta tcttctccat ggccacaggt tgaagcagcc cgaagactgc ctggatgaac 240
tgtatgaaat aatgtactct tgctggagaa ccgatccctt agaccgcccc accttttcag 300
tattgaggct gcagctagaa aaactcttag aaagtttgcc tgacgttcgg aaccaagcag 360
acgttattta cgtcaataca cagttgctgg agagctctga gggcctggcc agggctccac 420
ccttgctcca ctggacttga acatcgaccc tgactctata attgcctcct gcactccccg 480
cgctgccatc agtgtggtca cagcagaagt tcatgacagc aaacctcatg aaggacggta 540
catcctgaat gggggcagtg aggaatggga agatctgact tctgccccct ctgctgcagt 600
cacagctgaa aagaacagtg ttttaccggg ggagagactt gttaggaatg gggtctcctg 660
gtcccattcg agcatgctgc ccttgggaag ctcattgccc gatgaacttt gtttgctgac 720
gactcctcag aaggctcaga agtcctgatg tgaggagagg tgcggcgaga cattccaaaa 780
aatcaaagcc aattcttctg ctgtaggagg aatccaattg tacctgatgt            830
```

```
<210> 7
<211> 1126
<212> DNA
<213> Homo sapiens

<400> 7
gtgagccctt ggattctagc cagcacgact gaaggagccc catcagtagc acctttaaat 60
gtcactgtgt ttctgaatga atctagtgat aatgtggaca tcagatggat gaagcctccg 120
actaagcagc aggatggaga actggtgggc taccggatat cccacgtgtg gcagagtgca 180
gggatttcca aagagctctt ggaggaagtt ggccagaatg gcagccgagc tcggatctct 240
gttcaagtcc acaatgctac gtgcacagtg aggattgcag ccgtcaccag agggggagtt 300
gggcccttca gtgatccagt gaaaatattt atccctgcac acggttgggt agattatgcc 360
ccctcttcaa ctccggcgcc tggcaacgca gatcctgtgc tcatcatctt ggctgctttt 420
tgtggatttta tttcgattgg gttgatttta tacatctcct tggccatcag aaaaagagtc 480
caggagacaa agtttgggaa tgcattcaca gaggaggatt ctgaattagt ggtgaattat 540
ataagcaaca gaaatccttc tgttcggcga gccattgaac ttaccttaca tagcttggga 600
gtcagtgagg aactacaaaa taactaaacg atgtcgtgat tgacaggaat cttctaatct 660
tggacacact tctgggtgaa ggagagttgc gctccggact ggacaggcaa tcttcaagcc 720
agcaccatgg gacctctccc aaaattggcc tgaaaccttg aacgtcgcgc acacttcca 780
ccggcagacc cagcgatcac caccgacaga cgctcctgta agacttcagc ccgaattgtt 840
ccgcacactt acgacgcgcg gtactccaaa acaacaacca cagggaagtc acaaacacac 900
tggataataa acctgattca aagaagtggg acacgctgaa tactcagcat tattccgccg 960
```

- 13 -

```
tggccaacag accaacgatc gtcgcagcga ccaagaagca tcgcgcagct acgcctgagc 1020
agaatgtctc cacagatgat ctcaatcata ctgaaacgca ggcaagtaca tcatgcggaa 1080
gaccgaaaat actaatcagc atataagacc acaatcatat gatctc            1126
```

```
<210> 8
<211> 762
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(762)
<223> n = A,T,C or G

<400> 8
gacaggacca aagcatattc ctctgcagac actatggaag ttcatggtgg atattgccct 60
gggaatggag tatctgagca acaggaattt tcttcatcga gatttagctg ctcgaaactg 120
catcacccac ctggccatct tagcaagaag cccagcatct tgctcttact gcaggttgcg 180
agatgacatg actgtctgtg ttgcggactt cggcctctct aagaagattt acagtggcga 240
ttattaccgc caaggccgca ttgctaagat gcctgttaaa tggatcgcca tagaaagtct 300
tgcagaccga gtctacacaa gtaaaagtga tgtgtgggca tttggcgtga ccatgtggga 360
aatagctacg cggggaatga ctccctatcc tggggtccag aaccatgaga tgtatgacta 420
tcttctccat ggccacaggt tgaagcagcc cgaagactgc ctggatgaac tgtatgaaat 480
aatgtactct tgctggagaa ccgatccctt agaccgccca ccttttcagt attgaggctg 540
cagctagaaa aactcttaga aagtttgctg acgttcggaa ccaagcagac gttatttacg 600
tcaatacaca gttgctggag agctctgagg cctggccaan ggctcaccct tgcttcactg 660
gacttgaaca tcgacctgat ctattaattg cctctggatc ccggctgcat cagtgggtcc 720
cggcaagtta tggcagaact ctgaggggg aacctgaaag gg               762
```

```
<210> 9
<211> 602
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)...(602)
<223> n = A,T,C or G

<400> 9
ccttaccaca tctgtaccaa atcaagcagc tgcaagccct ggctaattac agcattggtg 60
tttcctgcat taatgaaata ggctggtctg cagtgagccc ttggattcta gccagcacga 120
ctgaaggagc cccatcagta gcacctttaa atgtcactgt gtttctgaat gaatctagtg 180
ataatgtgga catcagatgg atgaagcctc cgactaagca gcaggatgga gaactggtgg 240
gctaccggat atcccacgtg tggcanagtg cagggatttc caaagagctc ttggaggaag 300
ttggccagaa tggcagccga gctcggatct ctgttcaagt ccacaatgct acgtgcacag 360
tgaggattgc agccgtcacc aaagggggan ttgggccctt caatgatcca gtgaaaatat 420
ttatccctgc acacggttgg gtanattatg cccctcttc aactccggcg cctggcaacn 480
caaatcctgt gctcatcatc tttggctgct tttgtggatt tattttgatt gggttggttt 540
tatacatctc cttgggncat canaaaaana tccaggagac naatttgggg aatgccttcc 600
cn                                                       602
```

```
<210> 10
<211> 547
<212> DNA
<213> Homo sapiens

<400> 10
ggcgtgacca tgtgggaaat agctacgcgg ggaatgactc cctatcctgg ggtccagaac 60
```

- 14 -

```
catgagatgt atgactatct tctccatggc cacaggttga agcagcccga agactgcctg 120
gatgaactgt atgaaataat gtactcttgc tggagaaccg atcccttaga ccgccccacc 180
ttttcagtat tgaggctgca gctagaaaaa ctcttagaaa gtttgcctga cgttcggaac 240
caagcagacg ttatttacgt caatacacag ttgctggaga gctctgaggg cctggcccag 300
ggctccaccc ttgctccact ggacttgaac atcgaccctg actctataat tgcctcctgc 360
actccccgcg ctgccatcag tgtggtcaca gcagaagttc atgacagcaa acctcatgaa 420
ggacggtaca tcctgaatgg gggcagtgag gaatgggaag atctgacttc tgccccctct 480
gctgcagtca cagctgaaaa gaacagtgtt ttaccggggg agagacttgt taggaatggg 540
gtctcct                                                          547
```

```
<210> 11
<211> 633
<212> DNA
<213> Homo sapiens
```

```
<400> 11
tatgaatgaa ataggctggt ctgcagtgag cccttggatt ctagccagca cgactgaagg 60
agccccatca gtagcacctt taaatgtcac tgtgtttctg aatgaatcta gtgataatgt 120
ggacatcaga tggatgaagc ctccgactaa gcagacagga tggagaactg gtgggctacc 180
ggatatccca cgtgtggcag agtgcaggga tttccaaaga gctcttggag gaagttggcc 240
agaatggcag ccgagctcgg atctctgttc aagtccacaa tgctacgtgc acagtgagga 300
ttgcagccgt caccaaaggg ggagttgggc ccttcagtga tccagtgaaa atatttatcc 360
ctgcacacgg ttgggtagat tatgccccct cttcaactcc ggcgcctggc aacgcagatc 420
ctgtgctcat catctttggc tgcttatgtg gatttatata gataggttg gtttttataca 480
tctccttgga catcagaaaa agagtccagg agacaaagtc tgggaatgca ttcacagagg 540
aggattctga attagggtga cttatatagc aaagaaatcc ttctgtcgga gagccattga 600
acttacctta catagctagg gagtcagtga ggg                              633
```

```
<210> 12
<211> 635
<212> DNA
<213> Homo sapiens
```

```
<400> 12
gggaattcgg acttctggcc ggcagtttat ccgatttgaa gttacagaat aatcgcttcc 60
ttcagcataa ccagtgtgca gcgttcagac aatgggtcgt atatctgtaa gatgaaaata 120
aacaatgaag agatcgtgtc tgatcccatc tacatcgaag acaaggactt cctcacttta 180
ctaatcagtc tgagagcatg aatgtcacca gaaacacagc cttcaacctc tcctgtcagg 240
ctgtgggccc gcctgagccc gtcaacattt tctgggttca aaacagtagc cgtgttaacg 300
aacagcctga aaaatccccc tccgtgctaa ctgttccagg cctgacggag atggcggtct 360
tcagttgtga ggcccacaat gacaaagggc tgaccgtgtc caagggagtg cagatcaaca 420
tcaaagcaat tccctcccca ccaactgaag tcagcatccg taacaacact gcacacagca 480
ttctgatctc ctgggttcct ggttttgatg gatactcccc gttcaggaat tgcagcattc 540
aggtcaagga agctgatccg ctgagtaatg gctcagtcat gattttttac acctctgcct 600
taccacatct gtaccaaatc aagcagctgc aagcc                            635
```

```
<210> 13
<211> 766
<212> DNA
<213> Homo sapiens
```

```
<400> 13
cgtgaccatg tgggaaatag ctacgcgggg aatgactccc tatcctgggg tccagaacca 60
tgagatgtat gactatcttc tccatggcca caggttgaag cagcccgaag actgcctgga 120
tgaactgtat gaaataatgt actcttgctg gagaaccgat cccttagacc agcccacctt 180
ttcagtattg aggctgcagc tagaaaaact cttagaaagt ttgcctgacg ttcggaacca 240
agcagacgtt atttacgtca atacacagtt gctggagagc tctgagggcc tggcccaggg 300
ctccaccctt gctccactgg acttgaacat cgaccctgac tctataattg cctcctgcac 360
tccccgcgct gccatcagtg tggtcacagc agaagttcat gacagcaaac ctcatgaacg 420
```

- 15 -

```
gacggtacat cctgaatggg ggcagtgagg aatgggaaga tctgacttct gccccctctg 480
ctgcagtcac agctgaaaag aacagtgttt taccgggggga gagacttgtt aggaattggg 540
gtctcctggt cccattcgag catgctgccc ttgggaagct cattgccgat gaactttcgt 600
tgctgacgaa tcctcagaag gctcagaagt ctgatgtgag gaccaggtgc cgggaaaaca 660
ttccaaaaat caagcaaatc ttctgctgta ggaaaaccat tgttcctgat gtttcggcat 720
tgggctcctt aacaagtgaa ctcatgggcc aaaagaccag atgacc            766
```

```
<210> 14
<211> 616
<212> DNA
<213> Homo sapiens
```

```
<400> 14
agcggggaac aactcacttg tgtaagagac aaataccaaa aacatcaggt acaattggat 60
tctcctacag cagaagaatg ggcttgattt tgggaatgtc tccccgcacc tctcctcaca 120
tcaggacttc tgagccttct gaggagtcgt cagcaaacaa aagttcatcg ggcaatgagc 180
ttcccaaggg cagcatgctt gaatgggacc aggagacccc attcctaaca agtctctccc 240
ccggtaaaac actgttcttt tcagctgtga ctgcagcaga gggggcagaa gtcagatctt 300
cccattcctc agtgccccca ttcaggatgt accgtccttc atgaggtgtg ctgtcatgaa 360
cttctgctgt gaccacactg atggcagcgc ggggagtgca ggaggcaatt atagagtcag 420
ggtcgatgtt caagtccagt ggagcaaggg tggagccctg ggccaggccc tcagagctct 480
ccagcaactg tgtatagacg taaataatgt cggcttggtt ccgaacgtca ggcaaccttt 540
ctaagagttt atctagctgc agcctcaata ctgaaaaggt gggggcggtc tacgggatcg 600
gtctccagca agagtc                                               616
```

```
<210> 15
<211> 971
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)...(971)
<223> n = A,T,C or G
```

```
<400> 15
acctttcag ntattgaggc tgcagctaga aaaactctta gaaagtttgc ctgacgttcg 60
gaaccaagca gacgttattt acgtcaatac acagttgctg gagagctctg agggcctggc 120
ccaggctcc accettgctc cactggactt gaacatcgac cctgactcta taattgcctc 180
ctgcactccc cgcgctgcca tcagtgtggt cacagcagaa gttcatgaca gcaaacctca 240
tgaaggacgg tacatcctga atggggggcag tgaggaatgg gaagatctga cttctgcccc 300
ctctgctgca gtcacagctg aaaagaacag tgttttaccg ggggagagac ttgttaggaa 360
tggggtctcc tggtcccatt cgagcatgct gcccttggga agctcattgc cgatgaact 420
tttgtttgct gacgactcct cagaaggctc agaagtcctg atgtgaggag aggtgcgggg 480
agacattcca aaaatcaagc caattcttct gctgtaggag aatccaattg tacctgatgt 540
tttggtattt gtcttcctta ccaagtgaac tccatgngcc ccaaagcacc agatgaatgt 600
tgttaagtaa gctgtcatta aaaataccta atatatattt atttcaccga cgaaccccct 660
ctgtgtctct catggcagcc ccgaccagga ctctctaatt aaacatttct tatttcattt 720
cacttatctg ctattcttaa aattagctca gtggtctgat tttacacttg tcgagtgaag 780
ctgtttttcac ggcttctttt cggcataagg gcacacttgg cacgccagcc catgctgggc 840
ggccatgttt taacaagatc tcacgtgcag gtaaacgact acggggcgcg caccgaggaa 900
aagacgccat acggcgcccc ccgtagtcat acatagtccg aaattgggac acatgatgaa 960
attacatccc n                                                    971
```

```
<210> 16
<211> 484
<212> DNA
<213> Homo sapiens
```

```
<400> 16
aaaaactttt agaaagtttg cctgacgttc ggaaccaagc agacgttatt tacgtcaata 60
cacagttgct ggagagctct gagggcctgg cccagggctc cacccttgct ccactggact 120
tgaacatcga ccctgactct ataattgcct cctgcactcc ccgcgctgcc atcagtgtgg 180
tcacagcaga agttcatgac agcaaacctc atgaaggacg gtacatcctg aatgggggca 240
gtgaggaatg ggaagatctg acttctgccc cctctgctgc agtcacagct gaaaagaaca 300
gtgttttacc ggggggagaga cttgttagga atggggtctc ctggtcccat tcgagcatgc 360
tgcccttggg aagctcattg cccgatgaac ttttgtttgc tgacgactcc tcagaaggct 420
cagaagtcct gatgtgagga gaggtgcggg gagacattcc aaaaatcaag ccaattcttc 480
tgca                                                             484
```

```
<210> 17
<211> 431
<212> DNA
<213> Homo sapiens
```

```
<400> 17
ggatgaagcc tccgactaag cagcaggatg gagaactggt gggctaccgg atatcccacg 60
tgtggcagag tgcagggatt tccaaagagc tcttggagga agttggccag aatggcagcc 120
gagctcggat ctctgttcaa gtccacaatg ctacgtgcac agtgaggatt gcagccgtca 180
ccaaaggggg agttgggccc ttcagtgatc cagtgaaaat atttatccct gcacacggtt 240
gggtagatta tgccccctct tcaactccgg cgcctggcaa cgcagatcct gtgctcatca 300
tctttggctg ctcttgtgga tgtatattga ttgggttggt tttatacatc tacttggaca 360
tcagaaaaag agtccaggag acaaagtttg ggaatgcata cacagaggag gattctgaat 420
gagtggtgaa t                                                     431
```

```
<210> 18
<211> 24
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> random oligonucleotide
```

```
<400> 18
tcaactgact agatgtacat ggac                                        24
```

```
<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Primer1
```

```
<400> 19
cgtgttaacg aacagcctga                                             20
```

```
<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence
```

```
<220>
<223> Primer2
```

```
<400> 20
caactgaaga ccgccatctc                                             20
```

```
<210> 21
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Probe1

<400> 21
ccgtgctaac tgttccaggc ctgac                                              25
```